AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1. (Currently amended) A method for comparing nucleic acids, said method comprising:

(a) providing a first sample comprising a first population of first nucleic acids having different nucleotide sequences, and a second sample comprising a second population of second nucleic acids having different nucleotide sequences, wherein the nucleotide sequences of said second population are known;

(b) probing said first sample with one or more recognition means, each recognition means recognizing a target nucleotide subsequence or a set of target nucleotide subsequences, wherein if said first sample is probed with two or more recognition means, each recognition means recognizes a different target nucleotide subsequence or a different set of target nucleotide subsequences;

(c) generating one or more output signals from said first sample probed by said recognition means, each output signal comprising a representation of (i) the distance between occurrences of target nucleotide subsequences in said first nucleic acid, and (ii) the identities of said target nucleotide subsequences in said first nucleic acid or the identities of said sets of target nucleotide subsequences among which are included the target nucleotide subsequences in said first nucleic acid; and

(d) comparing each representation provided by said first sample with said second population by generating (i) a statistical score which states the probability that one or more output signals from said first sample indicates that one or more nucleotide sequences of said first sample are either present or absent in said second sample; and (ii) a statistical score of a false-negative rate or a false-positive rate, wherein said false-negative rate is a representation of the probability that said output from said first nucleic acid or said second nucleic acid is not generated given that said first or second nucleic acid is present, and said false-positive rate being a representation of the probability that said output from said first nucleic acid or said second nucleic acid is generated given that said first or second nucleic acid is not present.

2. (Original) The method of claim 1, wherein the output signals from said first sample indicate that one or more nucleotide sequences of said first sample are present in said second sample.

3. (Original) The method of claim 1, wherein the output signals from said first sample indicate that one or more nucleotide sequences of said first sample are absent in said second sample.

4. (Original) The method of claim 1, wherein said statistical score is generated according to Bayes Rule of conditional probability.

5. (Previously presented) The method of claim 1, wherein said distance between occurrences of target nucleotide subsequences is pre-determined.

6. (Currently amended) The method of claim 1, wherein said comparison is performed by ~~additionally generating a statistical score of the false-negative rate, said false-negative rate being a representation of the probability that said output from said first nucleic acid or said second nucleic acid is not generated given that said first or second nucleic acid is present~~ generating (i) a statistical score which states the probability that one or more output signals from said first sample indicates that one or more nucleotide sequences of said first sample are either present or absent in said second sample; and (ii) a statistical score of a false-negative rate.

7. (Currently amended) The method of claim 1, wherein said comparison is performed by ~~additionally generating a statistical score of the false-positive rate, said false-positive rate being a representation of the probability that said output from said first nucleic acid or said second nucleic acid is generated given that said first or second nucleic acid is not present~~ generating (i) a statistical score which states the probability that one or more output signals from said first sample indicates that one or more nucleotide sequences of said first sample are either present or absent in said second sample; and (ii) a statistical score of a false-positive rate.

8. (Currently amended) A method for comparing one or more nucleic acids, said method comprising:

(a) providing a first sample comprising a first population of first nucleic acids having different nucleotide sequences, and a second sample comprising a second population of second

nucleic acids having different nucleotide sequences, wherein the nucleotide sequences of said second population are not known;

(b) probing said first sample with one or more recognition means, each recognition means recognizing a target nucleotide subsequence or a set of target nucleotide subsequences, wherein if said first sample is probed with two or more recognition means, each recognition means recognizes a different target nucleotide subsequence or a different set of target nucleotide subsequences;

(c) generating one or more output signals from said first sample probed by said recognition means, each output signal comprising a representation of (i) the distance between occurrences of target nucleotide subsequences in said first nucleic acid, (ii) the identities of said target nucleotide subsequences in said first nucleic acid or the identities of said sets of target nucleotide subsequences among which are included the target nucleotide subsequences in said first nucleic acid; and (iii) a measure of the level/amount of the first nucleic acid in the first sample producing the output signal; ~~and~~

(d) performing steps (b) and (c) for said second sample; and

(e) comparing the representation provided by said first sample with the representation provided by the second sample by generating (i) a statistical score which states the probability that one or more output signals from said first sample indicates that one or more nucleotide sequences of said first sample are either present or absent in said second sample; and (ii) a statistical score of a false-negative rate or a false-positive rate, wherein said false-negative rate is a representation of the probability that said output from said first nucleic acid or said second nucleic acid is not generated given that said first or second nucleic acid is present, and said false-positive rate being a representation of the probability that said output from said first nucleic acid or said second nucleic acid is generated given that said first or second nucleic acid is not present.

9. (Original) The method of claim 8, wherein the output signals from said first sample indicate that one or more nucleotide sequences of said first sample are present in said second sample.

10. (Original) The method of claim 8, wherein the output signals from said first sample indicate that one or more nucleotide sequences of said first sample are absent in said second sample.

11. (Original) The method of claim 8, wherein said statistical score is generated according to Bayes Rule of conditional probability.

12. (Currently amended) ~~The method of claim 8,~~ A method for comparing one or more nucleic acids, said method comprising:

(a) providing a first sample comprising a first population of first nucleic acids having different nucleotide sequences, and a second sample comprising a second population of second nucleic acids having different nucleotide sequences, wherein the nucleotide sequences of said second population are not known;

(b) probing said first sample with one or more recognition means, each recognition means recognizing a target nucleotide subsequence or a set of target nucleotide subsequences, wherein if said first sample is probed with two or more recognition means, each recognition means recognizes a different target nucleotide subsequence or a different set of target nucleotide subsequences;

(c) generating one or more output signals from said first sample probed by said recognition means, each output signal comprising a representation of (i) the distance between occurrences of target nucleotide subsequences in said first nucleic acid, (ii) the identities of said target nucleotide subsequences in said first nucleic acid or the identities of said sets of target nucleotide subsequences among which are included the target nucleotide subsequences in said first nucleic acid; and (iii) a measure of the level/amount of the first nucleic acid in the first sample producing the output signal;

(d) performing steps (b) and (c) for said second sample; and

(e) comparing the representation provided by said first sample with the representation provided by the second sample by generating a statistical score which states the probability that one or more output signals from said first sample indicates that one or more nucleotide sequences of said first sample are either present or absent in said second sample; and wherein said statistical score is generated by:

i) performing steps (a) through (d) on two or more independent samples of said first and said second sample;

ii) generating an average representation of said independent samples; and

iii) generating a p-value from an f-test performed on said average representation.

13. (Original) The method of claim 12, wherein said p-value is between about 0.05 and about 0.10.

14. (Previously presented) The method of claim 12, wherein said distance between occurrences of target nucleotide subsequences is pre-determined.

15. (Previously presented) The method of claim 8, wherein said distance between occurrences of target nucleotide subsequences is pre-determined.

16. (Currently amended) The method of claim 8, wherein said comparison is performed by ~~additionally generating a statistical score of the false-negative rate, said false-negative rate being a representation of the probability that said output from said first nucleic acid or said second nucleic acid is not generated given that said first or second nucleic acid is present~~ generating (i) a statistical score which states the probability that one or more output signals from said first sample indicates that one or more nucleotide sequences of said first sample are either present or absent in said second sample; and (ii) a statistical score of a false-negative rate.

17. (Currently amended) The method of claim 8, wherein said comparison is performed by ~~additionally generating a statistical score of the false-positive rate, said false-positive rate being a representation of the probability that said output from said first nucleic acid or said second nucleic acid is generated given that said first or second nucleic acid is not present~~ generating (i) a statistical score which states the probability that one or more output signals from said first sample indicates that one or more nucleotide sequences of said first sample are either present or absent in said second sample; and (ii) a statistical score of a false-positive rate.

18. (Currently amended) A method for identifying or classifying one or more nucleic acids in a first sample comprising a first population of first nucleic acids having different nucleotide sequences, said method comprising:

(a) probing said first sample with one or more recognition means, each recognition means recognizing a target nucleotide subsequence or a set of target nucleotide subsequences, wherein if said first sample is probed with two or more recognition means, each recognition means recognizes a different target nucleotide subsequence or a different set of target nucleotide subsequences, and wherein the probing comprises the steps of (i) contacting the first sample with the recognition means to provide an amplification mixture, and (ii) conducting an amplification process on said amplification mixture;

(b) generating one or more output signals from said first sample probed by said recognition means, each output signal comprising a representation of (i) the distance between occurrences of target nucleotide subsequences in said first nucleic acid, and (ii) the identities of said target nucleotide subsequences in said first nucleic acid or the identities of said sets of target nucleotide subsequences among which are included the target nucleotide subsequences in said first nucleic acid; and

(c) comparing each representation provided by said first sample with a second population of second nucleic acids having different nucleotide sequences, wherein the different nucleotide sequences of said second population are known, by generating a statistical score which states the probability that one or more output signals from said first sample indicates that one or more nucleic acid sequences of said first sample are either present or absent in said second sample;

whereby said indication of presence or absence provides said identification or classification.

19. (Original) The method of claim 18, wherein the output signals from said first sample indicate that one or more nucleotide sequences of said first sample are present in said second sample.

20. (Original) The method of claim 18, wherein the output signals from said first sample indicate that one or more nucleotide sequences of said first sample are absent in said second sample.

21. (Currently amended) A method for identifying or classifying one or more nucleic acids in a first sample comprising a first population of first nucleic acids having different nucleotide sequences, said method comprising:

(a) probing said first sample with one or more recognition means, each recognition means recognizing a target nucleotide subsequence or a set of target nucleotide subsequences, wherein if said first sample is probed with two or more recognition means, each recognition means recognizes a different target nucleotide subsequence or a different set of target nucleotide subsequences, and wherein the probing comprises the steps of (i) contacting the first sample with the recognition means to provide an amplification mixture, and (ii) conducting an amplification process on said amplification mixture;

(b) generating one or more output signals from said first sample probed by said recognition means, each output signal comprising a representation of (i) the distance between occurrences of target nucleotide subsequences in said first nucleic acid, and (ii) the identities of said target nucleotide subsequences in said first nucleic acid or the identities of said sets of target nucleotide subsequences among which are included the target nucleotide subsequences in said first nucleic acid;

(c) performing steps (a) and (b) for a second population of second nucleic acids having different nucleotide sequences, wherein the different nucleotide sequences of said second population are not known;

(d) comparing each representation provided by said first sample with said second sample, by generating a statistical score which states the probability that one or more output signals from said first sample indicates that one or more nucleotide sequences of said first sample are either present or absent in said second sample;

whereby said indication of presence or absence provides said identification or classification.

22. (Original) The method of claim 21, wherein the output signals from said first sample indicate that one or more nucleotide sequences of said first sample are present in said second sample.

23. (Original) The method of claim 21, wherein the output signals from said first sample indicate that one or more nucleotide sequences of said first sample are absent in said second sample.

24. (Currently amended) A method for identifying, classifying, or quantifying one or more nucleic acids in a first sample comprising a first population of first nucleic acids having different nucleotide sequences, said method comprising:

(a) probing said first sample with one or more recognition means, each recognition means recognizing a target nucleotide subsequence or a set of target nucleotide subsequences, wherein if said first sample is probed with two or more recognition means, each recognition means recognizes a different target nucleotide subsequence or a different set of target nucleotide subsequences, and wherein the probing comprises the steps of (i) contacting the first sample with the recognition means to provide an amplification mixture, and (ii) conducting an amplification process on said amplification mixture;

(b) generating one or more output signals from said first sample probed by said recognition means, each output signal comprising a representation of (i) the distance between occurrences of target nucleotide subsequences in said first nucleic acid, (ii) the identities of said target nucleotide subsequences in said first nucleic acid or the identities of said sets of target nucleotide subsequences among which are included the target nucleotide subsequences in said first nucleic acid, and (iii) a measure of the level/amount of the first nucleic acid in the first sample producing the output signal; and

(c) comparing each representation provided by said first sample with a second population of second nucleic acids having different nucleotide sequences, wherein the different nucleotide sequences of said second population are known, by generating a statistical score which states the probability that one or more output signals from said first sample indicates that one or more nucleotide sequences of said first sample are either present or absent in said second sample;

whereby said indication of presence or absence provides said identification, classification, or quantitation.

25. (Original) The method of claim 24, wherein the output signals from said first sample indicate that one or more nucleotide sequences of said first sample are present in said second sample.

26. (Original) The method of claim 24, wherein the output signals from said first sample indicate that one or more nucleotide sequences of said first sample are absent in said second sample.

27. (Currently amended) A method for identifying, classifying, or quantifying one or more nucleic acids in a first sample comprising a first population of first nucleic acids having different nucleotide sequences, said method comprising:

(a) probing said first sample with one or more recognition means, each recognition means recognizing a target nucleotide subsequence or a set of target nucleotide subsequences, wherein if said first sample is probed with two or more recognition means, each recognition means recognizes a different target nucleotide subsequence or a different set of target nucleotide subsequences, and wherein the probing comprises the steps of (i) contacting the first sample

with the recognition means to provide an amplification mixture, and (ii) conducting an amplification process on said amplification mixture;

(b) generating one or more output signals from said first sample probed by said recognition means, each output signal comprising a representation of (i) the distance between occurrences of target nucleotide subsequences in said first nucleic acid, (ii) the identities of said target nucleotide subsequences in said first nucleic acid or the identities of said sets of target nucleotide subsequences among which are included the target nucleotide subsequences in said first nucleic acid, and (iii) a measure of the level/amount of the first nucleic acid in the first sample producing the output signal;

(c) performing steps (a) and (b) for a second population of second nucleic acids having different nucleotide sequences, wherein the different nucleotide sequences of said second population are not known; and

(d) comparing each representation provided by said first sample with said second sample, by generating a statistical score which states the probability that one or more output signals from said first sample indicates that one or more nucleotide sequences of said first sample are either present or absent in said second sample;

whereby said indication of presence or absence provides said identification, classification or quantitation.

28. (Original) The method of claim 27, wherein the output signals from said first sample indicate that one or more nucleotide sequences of said first sample are present in said second sample.

29. (Original) The method of claim 27, wherein the output signals from said first sample indicate that one or more nucleotide sequences of said first sample are absent in said second sample.

30. (Original) The method of any of claims 18, 21, 24 or 27, wherein said statistical score is generated according to Bayes Rule of conditional probability, wherein said statistical score is related to the conditional probability that one or more second nucleic acids from said second population occurs in said first population when one or more representations of a first set of said first nucleic acids are present in said one or more output signals and no representation of a second set of first nucleic acids is present in said one or more output signals.

31. (Original) The method of any of Claims 18, 21, 24 or 27, wherein said indication that one or more nucleotide sequences of said first sample is present in said second sample is established when the conditional probability that an output signal is detected when no second nucleic acid is present in said second population is less than a predetermined limit.

32. (Original) The method of claim 31, wherein said predetermined limit is less than about 0.1.

33. (Original) The method of claim 31, wherein said predetermined limit is less than about 0.01.

34. (Original) The method of claim 31, wherein said predetermined limit is less than about 0.001.

35. (Original) The method described in any of claims 18, 21, 24 or 27, wherein the recognition means comprises one or more restriction endonucleases and the probing comprises contacting said first sample with said recognition means.

36. (Currently amended) The method described in any of claims 18, 21, 24 or 27, wherein the recognition means comprises one or more oligonucleotides of defined sequence~~, and the probing comprises the steps of~~

~~(a) contacting the first sample with the recognition means to provide an amplification mixture; and~~

~~(b) conducting an amplification process on said amplification mixture~~.

37-39. (Canceled).